UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/024,066	12/18/2001	Loren J. Field	7037-450	3713

7590   07/20/2005

Kenneth A. Gandy
Woodard, Emhardt, Naughton, Moriarty & McNett
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Indianapolis, IN 46204-5137

EXAMINER
SULLIVAN, DANIEL M

ART UNIT	PAPER NUMBER
1636	

DATE MAILED: 07/20/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

PTO-90C (Rev. 10/03)

		Application No.	Applicant(s)
Office Action Summary		10/024,066	FIELD ET AL.
		Examiner	Art Unit	
		Daniel M. Sullivan	1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE <u>3</u> MONTH(S) FROM
THE MAILING DATE OF THIS COMMUNICATION.
- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed
  after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
  Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any
  earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on <u>06 July 2005</u>.

2a)☐ This action is **FINAL**.   2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is
closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) <u>51 and 52</u> is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) <u>51 and 52</u> is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All   b)☐ Some *   c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage
application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1)☒ Notice of References Cited (PTO-892)

2)☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)

3)☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date _____.

4)☒ Interview Summary (PTO-413)
Paper No(s)/Mail Date. <u>7/12/05</u>.

5)☐ Notice of Informal Patent Application (PTO-152)

6)☒ Other: <u>sequence alignments</u>.

DETAILED ACTION

This Non-Final Office Action is a response to the Paper filed 6 July 2005 in response to the Final Office Action mailed 8 February 2005. Claims 43-59 and 63-84 had been withdrawn from consideration and claims 20-28, 49, 50 and 51-62 were considered in the 8 February Office Action. Claims 20-28, 49, 50, 53-62 and 63-84 were canceled and claims 51 and 52 were amended in the 6 July Paper. Claims 51 and 52 are pending.

Finality of the previous Office Action is hereby **withdrawn** in view of the new grounds for rejection set forth herein below.

Response to Amendment

Rejection of claims 20-28, 49, 50 and 53-62 is rendered moot by the cancellation thereof.

Objection to claims 51 and 52 is withdrawn in view of the amendments thereto.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

The factual inquiries set forth in *Graham* v. *John Deere Co.*, 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

1.   Determining the scope and contents of the prior art.
2.   Ascertaining the differences between the prior art and the claims at issue.
3.   Resolving the level of ordinary skill in the pertinent art.
4.   Considering objective evidence present in the application indicating obviousness
        or nonobviousness.

This application currently names joint inventors. In considering patentability of the

claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various

claims was commonly owned at the time any inventions covered therein were made absent any

evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out

the inventor and invention dates of each claim that was not commonly owned at the time a later

invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c)

and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claim 51 is rejected under 35 U.S.C. 103(a) as being unpatentable over Soonpaa *et al.*

(1997) *J. Clin. Invest.* 99:2644 (previously made of record) in view of Li *et al.* (1998) *Am. J.*

Physiol. 275:H814-H822 and further in view of ENTREZ Nucleotide Database Entry Accession

No. M86182 (hereinafter, M86182).

The claim is directed to a cardiomyocyte cell including an introduced nucleic acid

molecule wherein the molecule encodes the polypeptide set forth as SEQ ID NO: 2.

Soonpaa *et al.* teaches overexpression of a cyclin D protein in cardiomyocytes of a

transgenic mouse (see especially the paragraph bridging the left and right columns on page 2645

and the paragraph bridging the left and right columns on page 2647).

Soonpaa does not teach overexpression of an introduced nucleic acid encoding a nucleic

acid comprising the amino acid sequence of SEQ ID NO: 2. However, Soonpaa *et al.* teaches,

"[g]iven the therapeutic potential of regenerative myocardial growth, considerable effort has

been invested to develop strategies to induce cardiomyocyte proliferation" (first full paragraph in the left column on page 2644) and "[t]his study represents an initial pragmatic effort to test candidate genes which may participate in the regulation of cardiomyocyte DNA synthesis" (third paragraph on page 2645).

Li *et al.* teaches that cyclin D2 is upregulated during cardiomyocyte hypertrophic growth (see especially the Abstract, the paragraph bridging pages H816-H817, Figure 2 and the caption thereto). Li *et al.* concludes, "[f]uture experiments designed to induce forced expression of these [including cyclin D2] molecules in cardiomyocytes should offer an approach to determine the precise role of cell cycle regulatory molecules in cardiomyocyte hypertrophy and may lead to strategies for improving the prognosis of this disease" (paragraph bridging pages H821-H822).

M86182 teaches a cyclin D2 nucleic acid encoding the instant SEQ ID NO: 2 (see the attached sequence alignment).

It would have been obvious to one of ordinary skill in the art at the time the invention was made to produce a transgenic mouse according to the teachings of Soonpaa *et al.* using the cyclin D2 nucleic acid disclosed in M86182 the cardiomyocytes of which would be the same as the cardiomyocytes of the instant claims. Motivation to combine these teachings comes from Soonpaa *et al.*, who teaches the desirability of identifying regulators of cardiomyocyte proliferation and that the transgenic animal disclosed therein provides a means to test candidate genes that may participate in regulation of cardiomyocyte DNA synthesis. Further motivation comes from the teachings of Li *et al.*, which establish the upregulation of cyclin D2 during cardiomyocyte hypertrophic growth and teach that forced overexpression of genes upregulated in hypertrophy should offer an approach to determine the role of these genes and may lead to

therapeutic strategies. Thus, the skilled artisan would clearly be motivated to make a mouse

comprising a nucleic acid encoding the instant SEQ ID NO:.2 as disclosed in M86182.

Absent evidence to the contrary, one would have a reasonable expectation of success in

combining these teachings in view of the well-established nature of transgenic animal technology

and the guidance for making a transgenic animal expressing a cyclin D protein provided in

Soonpaa *et al.*

For these reasons, the invention of claim 51, as a whole, would have been obvious to one

of ordinary skill in the art at the time the invention was made.

Claim 52 is rejected under 35 U.S.C. 103(a) as being unpatentable over Soonpaa *et al.*

(1997) *J. Clin. Invest.* 99:2644 (previously made of record) in view of Li *et al.* (1998) *Am. J.*

Physiol. 275:H814-H822 and further in view of ENTREZ Nucleotide Database Entry Accession

No. X68452 (hereinafter, X68452).

The claim is directed to a cardiomyocyte cell including an introduced nucleic acid

molecule wherein the molecule encodes the polypeptide set forth as SEQ ID NO: 4.

Soonpaa *et al.* teaches overexpression of a cyclin D protein in cardiomyocytes of a

transgenic mouse (see especially the paragraph bridging the left and right columns on page 2645

and the paragraph bridging the left and right columns on page 2647).

Soonpaa does not teach overexpression of an introduced nucleic acid encoding a nucleic

acid comprising the amino acid sequence of SEQ ID NO: 4. However, Soonpaa *et al.* teaches,

"[g]iven the therapeutic potential of regenerative myocardial growth, considerable effort has

been invested to develop strategies to induce cardiomyocyte proliferation" (first full paragraph in

the left column on page 2644) and "[t]his study represents an initial pragmatic effort to test

candidate genes which may participate in the regulation of cardiomyocyte DNA synthesis" (third

paragraph on page 2645).

Li *et al.* teaches that cyclin D2 is upregulated during cardiomyocyte hypertrophic growth

(see especially the Abstract, the paragraph bridging pages H816-H817, Figure 2 and the caption

thereto). Li *et al.* concludes, "[f]uture experiments designed to induce forced expression of these

[including cyclin D2] molecules in cardiomyocytes should offer an approach to determine the

precise role of cell cycle regulatory molecules in cardiomyocyte hypertrophy and may lead to

strategies for improving the prognosis of this disease" (paragraph bridging pages H821-H822).

X68452teaches a cyclin D2 nucleic acid encoding the instant SEQ ID NO: 4 (see the

attached sequence alignment).

It would have been obvious to one of ordinary skill in the art at the time the invention

was made to produce a transgenic mouse according to the teachings of Soonpaa *et al.* using the

cyclin D2 nucleic acid disclosed in X68452, the cardiomyocytes of which would be the same as

the cardiomyocytes of the instant claims. Motivation to combine these teachings comes from

Soonpaa *et al.*, who teaches the desirability of identifying regulators of cardiomyocyte

proliferation and that the transgenic animal disclosed therein provides a means to test candidate

genes that may participate in regulation of cardiomyocyte DNA synthesis. Further motivation

comes from the teachings of Li *et al.*, which establish the upregulation of cyclin D2 during

cardiomyocyte hypertrophic growth and teach that forced overexpression of genes upregulated in

hypertrophy should offer an approach to determine the role of these genes and may lead to

therapeutic strategies. Thus, the skilled artisan would clearly be motivated to make a mouse

comprising a nucleic acid encoding the instant SEQ ID NO: 4 as disclosed in X68452.

Absent evidence to the contrary, one would have a reasonable expectation of success in

combining these teachings in view of the well-established nature of transgenic animal technology

and the guidance for making a transgenic animal expressing a cyclin D protein provided in

Soonpaa *et al.*

For these reasons, the invention of claim 52, as a whole, would have been obvious to one

of ordinary skill in the art at the time the invention was made.

Conclusion

Any inquiry concerning this communication or earlier communications from the
examiner should be directed to Daniel M Sullivan whose telephone number is 571-272-0779.
The examiner can normally be reached on Monday through Friday 6:30-3:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's
supervisor, Remy Yucel, Ph.D. can be reached on 571-272-0781. The fax phone number for the
organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent
Application Information Retrieval (PAIR) system. Status information for published applications
may be obtained from either Private PAIR or Public PAIR. Status information for unpublished
applications is available through Private PAIR only. For more information about the PAIR
system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR
system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Daniel M. Sullivan, Ph.D.
Examiner
Art Unit 1636

DANIEL M. SULLIVAN
PATENT EXAMINER

Qy   261 TyrArgGlnAspGlnArgAspGlySerLysSerGluAspGlnAlaSerThr 280
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Db   936 TACCGTCAGGACCAACGTGCGGATCGGAGGATGAACTCGGACCAAGCCAGCACC 995

Qy   281 ProThrAspValArgAspIleAspLeu 289
          ||||||||||||||||||||||||||
Db   996 CCTACAGACGTGCGGGATATCGACCTG 1022

RESULT 3
HSCYCD2
LOCUS   HSCYCD2   1129 bp   mRNA   linear   PRI 30-MAR-1993
DEFINITION H.sapiens mRNA for cyclin D2.
ACCESSION   X68452
VERSION   X68452.1   GI:38415
KEYWORDS   binding protein; CCND2 gene; cyclin D2; protein kinase.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1129)
AUTHORS   Palmero,I., Holder,A., Sinclair,A.J., Dickson,C. and Peters,G.
TITLE   Cyclins D1 and D2 are differentially expressed in human B-lymphoid
            cell lines
JOURNAL   Oncogene 8 (4), 1049-1054 (1993)
MEDLINE   93205384
PUBMED   8455931
REFERENCE   2 (bases 1 to 1129)
AUTHORS   Peters,G.
TITLE   Direct Submission
JOURNAL   Submitted (17-SEP-1992) G. Peters, Imperial Cancer Research Fund,
            P.O.Box 123, Lincoln's Inn Fields, London WC2A 3PX, UK
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                     EHILRKLPQQREKLSLIRKHAQFIALCATDFKFAMYPPSMIATGSVGAAICGLQQDE
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ORIGIN
Alignment Scores:
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Score: 1501.00   Matches: 289
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: Gaps: 0

US-10-024-066-4 (1-289) x HSCYCD2 (1-1129)

Qy   1 MetGluLeuLeuCysHisGluValAspProValArgArgAlaValArgAspArgAsnLeu 20
          ATGGAGCTGCTGTGCCACGAGGTGGACCCCGTGCGTCCGAGGGCCGTCCGGGACCGCAACCTG 215
Db   156 ATGGAGCTGCTGTGCCACGAGGTGGACCCCGTGCGTCCGAGGGCCGTCCGGGACCGCAACCTG 215

Qy   21 LeuArgAspAspArgValLeuGlnAsnLeuLeuThrIleGluGluArgTyrLeuProGln 40

Db   216 CTCCGAGACGACCGCGTCCTGCAGAACCTGCTCACCATCGAGGAGCGCTACCTTCCGCAG 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   41 CysSerTyrPheLysCysValGlnLysAspIleGlnProTyrMetArgArgMetValAla 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   61 ThrTrpMetLeuValCysGluGluGlnLysCysGluGluGluValPheProLeuAla 80
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Qy   81 MetAsnTyrLeuAspArgPheLeuAlaGlyValProThrProLysSerHisLeuGlnLeu 100
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Qy   101 LeuGlyAlaValCysMetPheLeuAlaSerLysLeuLysGluThrSerProLeuThrAla 120
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Qy   121 GluLysLeuCysIleTyrThrAspAsnSerIleLysProGlnLeuLeuGluTrpGlu 140
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Qy   141 LeuValValLeuGlyLysLeuLysTrpAsnLeuAlaAlaValThrProHisAspPheIle 160
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Qy   161 GluHisIleLeuArgLysLeuProGlnGlnArgGluLysLeuSerLeuIleArgLysHis 180
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Qy   181 AlaGlnPheIleAlaLeuCysAlaThrAspPheLysPheAlaMetTyrProProSer 200
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Qy   201 MetIleAlaThrGlySerValGlyAlaAlaIleCysGlyLeuGlnGlnAspGluGluVal 220
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Qy   221 SerSerLeuThrCysAspAlaLeuThrGluLeuLeuAlaLysIleThrAsnThrAspVal 240
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Qy   241 AspCysLeuLysAlaCysGlnGluGlnIleGluAlaValLeuLeuAsnSerLeuGlnGln 260
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Qy   261 TyrArgGlnAspGlnArgAspGlySerLysSerGluAspGlnAlaSerThr 280
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   936 TACCGTCAGGACCAACGTGCGGATCGGAGGATGAACTCGGACCAAGCCAGCACC 995

Qy   281 ProThrAspValArgAspIleAspLeu 289
          ||||||||||||||||||||||||||
Db   996 CCTACAGACGTGCGGGATATCGACCTG 1022

RESULT 4
BC010958
LOCUS   BC010958   1344 bp   mRNA   linear   PRI 29-JUN-2004
DEFINITION Homo sapiens cyclin D2, mRNA (cDNA clone MGC:13641 IMAGE:4136211),
            complete cds.
ACCESSION   BC010958
VERSION   BC010958.1   GI:15012104
KEYWORDS   MGC.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1344)
AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

US-10-024-066-2 (1-289) x AX695627 (1-1255)

```
Qy    1 MetGluLeuCysGlyCysGluValAspProValArgArgAlaValProAspArgAsnLeu  20
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Db  271 ATGGAGCTGTGTGGCTGTGGAGTCGAGGTGGACCCGGTTCCGCAGGGCCCGTGCCCAACCTG  330

Qy   21 LeuGluArgArgValLeuGlnAsnLeuThrIleGluThrHisThrIleGluProGlnCys  40
          | | | | | | | | | | | | | | | | | | | |
Db  331 CTGGAAGAACCCGGTTCTGCAGAACCTGTTGACCATCGAGACGAGCGCTACCTCCCGCAGTGT  390

Qy   41 SerTyrPheLysCysValGlnLysAspIleGlnProTyrMetArgArgMetValAlaThr  60
          | | | | | | | | | | | | | | | | | | | |
Db  391 TCCTATTTCAAGTGCGTGCAGAAGGACATCCAACCGTACATGCGCAGGATGGTGGCCACC  450

Qy   61 TrpMetLeuGluValCysGluGlnGlnLysCysGluGluGlnValPheProLeuAlaMet  80
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Db  451 TGGATGCTAGAGGTCTGTGAGCAACAAAAGTGTGAAGAGCAAGTCTTTCCTCTGGCCATG  510

Qy   81 AsnTyrLeuAspArgPheLeuAlaGlyValProThrProLysThrHisLeuGlnLeuLeu 100
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Db  511 AATTACCTGGACCGGTTTCTTGGCTGGAGTCCGACTCCCAAGACCCATCTTCAGCTCCTG  570

Qy  101 GlyAlaValCysMetPheLeuAlaSerLysLeuLysGluThrIleProLeuThrAlaGlu 120
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Db  571 GGTGCAGTGTGCATGTTCCTAGCTTCCAAGCTGAAAGAGACCATCCCGCTGACTGCGGAA  630

Qy  121 LysLeuCysIleTyrThrAspAsnSerValLysProGlnLeuLeuGluTrpGluLeu 140
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Db  631 AAGCTGTGCATTTACACCGACAACTCTGTGAAGCCCCAGGAGCTGCTGGAGTGGGAACTG  690

Qy  141 ValValLeuGlyLysLeuLysTrpAspLeuAlaAlaValThrProHisAspPheIleGlu 160
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Db  691 GTAGTGTTGGGTAAGCTGAAGTGGGACCTGGCAGCTGTCACCCCTCACGACTTCATTGAG  750

Qy  161 HisIleLeuArgLysLeuProGlnLeuLeuLeuArgLeuSerLeuIleArgLysHisAla 180
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Db  751 CACATCCTTCGCCAAGCTGCCCCAGCAAAAGGAGAGAAGCTGTCCCGATCCGCAAGCATGCG  810

Qy  181 GlnThrPheIleAlaLeuCysAlaThrAspPheLysPheAlaMetTyrProProSerMet 200
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Db  811 CAGACCTTCATCGCTCTGTGCGCTACCGACTTCAAGTTTGCCATGTACCCGCCATCGATG  870

Qy  201 IleAlaThrGlySerValGlyAlaAlaIleCysGlyLeuGlnLeuAspAspValAsn 220
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Qy  221 ThrLeuThrCysAspAlaLeuThrProGluLeuLeuAlaLysIleThrHisThrValAsp 240
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Db  931 ACACTCACGTGTGATGCCCTGACTCCAGAGCTGCTGGCCAAGATCACCCACACTGATGTGGAT  990

Qy  241 CysLeuLysAlaCysGlnGlnGlnIleGluAlaAlaLeuLeuAsnSerLeuGlnGlnPhe 260
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Db 1051 CGTCAAGAGCAGCATAACGCCGGATCCAAGTCTGTGGAAGATCCGGACCAAGCCACCACC 1110

Qy  281 ProThrAspValArgAspValAspLeu 289
          | | | | | | | | |
Db 1111 CCTACAGACGTGCGGGATGTTGACCTG 1137
```

RESULT 4

LOCUS   MUSDCYC   1255 bp   mRNA   linear   ROD 27-APR-1993

DEFINITION   Mouse D-type cyclin (CYL2) mRNA, complete cds.

ACCESSION   M83749

VERSION   M83749.1   GI:192938

KEYWORDS   D-type cyclin.

SOURCE   Mus musculus (house mouse)

  ORGANISM   Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Db  405 AATTACCTGGACCGGTTTCTTGGCTGGAGTCCGACTCCCAAGACCCATCTTCAGCTCCTG  464

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Qy  121 LysLeuCysIleTyrThrAspAsnSerValLysProGlnLeuLeuGluTrpGluLeu 140
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Qy  141 ValValLeuGlyLysLeuLysTrpAspLeuAlaAlaValThrProHisAspPheIleGlu 160
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Qy  161 HisIleLeuArgLysLeuProGlnLeuLeuLeuArgLeuSerLeuIleArgLysHisAla 180
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Qy  221 ThrLeuThrCysAspAlaLeuThrProGluLeuLeuAlaLysIleThrHisThrValAsp 240
Db  825 ACACTCACGTGTGATGCCCTGACTCCAGAGCTGCTGGCCAAGATCACCCACACTGATGTGGAT  884

Qy  241 CysLeuLysAlaCysGlnGlnGlnIleGluAlaAlaLeuLeuAsnSerLeuGlnGlnPhe 260
Db  885 TGTCTCAAAGCCTGCCAGGAGCAAATCGAAGCTGCTCTGCTGAACAGCCTGCAGCAGTTC  944

Qy  261 ArgGlnGluGlnHisAsnAlaGlySerLysSerValGluAspProAspGlnAlaThrThr 280
Db  945 CGTCAAGAGCAGCATAACGCCGGATCCAAGTCTGTGGAAGATCCGGACCAAGCCACCACC 1004

Qy  281 ProThrAspValArgAspValAspLeu 289
Db 1005 CCTACAGACGTGCGGGATGTTGACCTG 1031
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RESULT 3

LOCUS   AX695627   1255 bp   DNA   linear   PAT 31-MAR-2003

DEFINITION   Sequence 1254 from Patent WO03008583.

ACCESSION   AX695627

VERSION   AX695627.1   GI:29418779

KEYWORDS   .

SOURCE   Mus musculus (house mouse)

  ORGANISM   Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE   1

  AUTHORS   Morris,D.W. and Engelhard,E.K.

  TITLE   Novel compositions and methods for cancer

  JOURNAL   Patent: WO 03008583-A 1254 30-JAN-2003;
               Sagres Discovery (US)

FEATURES   Location/Qualifiers

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DB: Gaps: 0

US-10-024-066-2 (1-289) x AX695628 (1-870)

ORGANISM   Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1034)
  AUTHORS Matsushime,H., Roussel,M.F., Ashmun,R.A. and Sherr,C.J.
  TITLE   Colony-stimulating factor 1 regulates novel cyclins during the G1
           phase of the cell cycle
  JOURNAL Cell 65 (4), 701-713 (1991)
  MEDLINE 91235305
   PUBMED 1827757
REFERENCE 2 (bases 1 to 1034)
  AUTHORS Matsushime,H., Roussel,M.F. and Sherr,C.J.
  TITLE   Novel mammalian cyclin (CYL genes) expressed during G1
  JOURNAL Unpublished
COMMENT   Original source text: Mus musculus (sub_species domesticus) cDNA to
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FEATURES   Location/Qualifiers
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ORIGIN

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US-10-024-066-2 (1-289) x MUSCYL2A (1-1034)

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Db  165 ATGGAGCTGCTGTGTGCAGAGGTCGACCCGGTCGCGAGGTGGACCCCGGTCCGCAGGGCCGTGCCGGACCGCAACCTG 224

Qy   21 LeuGluAspArgValLeuGlnAsnLeuLeuThrIleGluAsnLeuLeuArgTyrLeuProGlnCys  40
          |||||||||||||||||||||||||||||
Db  225 CTGGAAGACACCCGGTCTCGCAGAACCTGTTGACCATCGAGGAACCATCGAGGAGCGCTACCTCCCCGCAGTGT 284

Qy   41 SerTyrPheLysCysValGlnValGlnLysAspIleGlnProTyrMetArgArgMetValAlaThr  60
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Db 421 GTAGTGTTGGGTAAGCTGAAGTGGAACCTGGCCGCAGTGACCCCTCACGACTTCATTGAG 480

Qy 161 HisIleLeuArgLysLeuProGlnGlnLysGluLysLeuSerLeuIleArgLysHisAla 180
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Qy 201 IleAlaThrGlySerValGlyAlaAlaIleCysGlyLeuGlnGlnAspAspGluValAsn 220
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Qy 241 CysLeuLysAlaCysGlnGluGlnIleGluAlaLeuLeuAsnSerLeuGlnGlnPhe 260
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Qy 281 ProThrAspValArgAspValAspLeu 289
Db 841 CCTACAGACGTGCGGGATGTGTGACCTG 867

RESULT 2
MUSCYL2A
LOCUS   MUSCYL2A   1034 bp   mRNA   linear   ROD 27-APR-1993
DEFINITION Mouse cyclin 2 (CYL 2) mRNA, complete cds.
ACCESSION   M86182
VERSION   M86182.1 GI:192879
KEYWORDS   cyclin 2.
SOURCE   Mus musculus (house mouse)

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2005. Compugen Ltd.

Run on: July 13, 2005, 23:40:22 ; Search time 669.5 Seconds
(without alignments)
2710.137 Million cell updates/sec

Title: US-10-024-066-2
Perfect score: 1513
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	1513	100.0	1255	11	US-09-997-722-2	Sequence 2, Appli
4	1380	91.2	870	13	US-09-997-722-6	Sequence 6, Appli
5	1380	91.2	873	13	US-10-024-066-3	Sequence 3, Appli
6	1380	91.2	1898	16	US-10-210-120-14	Sequence 14, Appl
7	1380	91.2	1898	22	US-10-909-035-14	Sequence 14, Appl
8	1380	91.2	1911	18	US-10-641-643-1022	Sequence 1022, Ap
9	1380	91.2	6478	9	US-09-919-497-4	Sequence 4, Appli
10	1380	91.2	6478	9	US-09-954-456-1923	Sequence 1923, Ap
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; Sequence 3, Application US/09997722
; Publication No. US2004007215A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301

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                    GenCore version 5.1.6

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OM protein - nucleic search, using frame_plus_p2n model


Run on:    July 13, 2005, 20:22:56 ; Search time 189 Seconds
                                   (without alignments)
                                   2502.032 Million cell updates/sec

Title:         US-10-024-066-2
Perfect score: 1513
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Total number of hits satisfying chosen parameters:      2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                         SUMMARIES
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5	1380	91.2	6478	4	US-09-949-016-256	Sequence 256, App
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8	1357	89.7	1970	3	US-08-463-772-3	Sequence 3, Appli
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12	975.5	64.5	1462	3	US-08-463-772-30	Sequence 30, Appl
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18	958	63.3	4244	1	US-08-460-744-1	Sequence 1, Appli
19	958	63.3	4244	3	US-07-667-711B-1	Sequence 1, Appli
20	957	63.3	4453	1	US-08-770-761A-4	Sequence 4, Appli
21	957	63.3	4540	1	US-08-770-761A-6	Sequence 6, Appli
22	957	63.3	4621	1	US-08-770-761A-1	Sequence 1, Appli
23	951.5	62.9	1462	5	PCT-US93-05000-30	Sequence 30, Appl
24	946	62.5	1325	1	US-08-306-691B-51	Sequence 51, Appl
25	916.5	60.6	1962	2	US-08-246-361A-5	Sequence 5, Appli
26	916.5	60.6	1962	4	US-09-023-655-1023	Sequence 1023, Ap
27	916.5	60.6	2042	4	US-09-814-915A-59	Sequence 59, Appl
28	892	59.0	1325	2	US-08-464-517-1	Sequence 1, Appli
29	892	59.0	1325	3	US-08-246-361A-1	Sequence 1, Appli
30	892	59.0	1325	3	US-08-463-772-1	Sequence 1, Appli
31	892	59.0	1325	5	PCT-US93-05000-1	Sequence 1, Appli
32	810.5	53.6	1926	2	US-08-464-517-5	Sequence 5, Appli
33	810.5	53.6	1926	3	US-08-463-772-5	Sequence 5, Appli
34	810.5	53.6	1926	5	PCT-US93-05000-5	Sequence 5, Appli
35	518.5	34.3	2022	2	US-08-464-517-32	Sequence 32, Appl
36	518.5	34.3	2022	2	US-08-246-361A-32	Sequence 32, Appl
37	518.5	34.3	2022	3	US-08-463-772-32	Sequence 32, Appl
38	428.5	28.3	1901	5	PCT-US93-05000-32	Sequence 32, Appl
39	372.5	24.6	36302	2	US-09-949-016-11998	Sequence 11998, A
40	372.5	24.6	36302	4	US-09-949-016-13891	Sequence 13891, A
41	321.5	21.2	863	2	US-08-728-603-18	Sequence 18, Appl
c 42	321.5	21.2	32207	2	US-08-770-379-20	Sequence 20, Appl
c 43	321.5	21.2	32207	3	US-08-757-669A-20	Sequence 20, Appl
c 44	321.5	21.2	32207	3	US-09-230-371A-20	Sequence 20, Appl
45	276	18.2	601	4	US-09-949-016-23242	Sequence 23242, A

```
                         ALIGNMENTS

RESULT 1
US-09-920-760-3
; Sequence 3, Application US/09920760
; Patent No. 6492173
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN D2 EXPRESSION
;  FILE REFERENCE: RTS-0275
;  CURRENT APPLICATION NUMBER: US/09/920,760
;  CURRENT FILING DATE: 2001-08-01
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
;  LENGTH: 1129
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (156)...(1025)
US-09-920-760-3

Alignment Scores:
Pred. No.:                  3.15e-180      Length:           1129
Score:                      1380.00        Matches:          266
Percent Similarity:         97.24%         Conservative:     16
Best Local Similarity:      91.72%         Mismatches:       6
Query Match:                91.21%         Indels:           6
DB:                         4              Gaps:             2

US-10-024-066-2 (1-289) x US-09-920-760-3 (1-1129)

Qy     1 MetGluLeuLeuCysCysGluValAspProValArgArgAlaValProAspArgAsnLeu 20
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   156 ATGGAGCTGCTGTGCTGCGAGGTGCCACGAGGTGGACCCGGTCCGCAGGGCCGTGCCGGACCGCAACCTG 215

Qy    21 Leu---GluAspArgValLeuGlnAsnLeuLeuThrIleGluGluArgTyrLeuProGln 39
           |||       :::|||||||||||||||||||||||||||||||||||||||||||||
```

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 13, 2005, 17:34:44 ; Search time 596.5 Seconds
(without alignments)
2868.072 Million cell updates/sec

Title: US-10-024-066-2
Perfect score: 1513
Sequence: 1 MELLCCEVDPVRRAVPDRNL.........KSVEDPDQATTPTDVRDVDL 289

Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop 6.0 , Fgapext 7.0
                Delop   6.0 , Delext   7.0

Searched: 439020 6 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10024066/runat_13072005_140959_28036/app_query.fasta_1.910
-DB=N Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=pct -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10024066 @CGN_1_1_586 @runat_13072005_140959_28036 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=0 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq_16Dec04:*
            1: geneseqm1980s:*
            2: geneseqm1990s:*
            3: geneseqm2000s:*
            4: geneseqm2001as:*
            5: geneseqm2001bs:*
            6: geneseqm2002as:*
            7: geneseqm2002bs:*
            8: geneseqm2003as:*
            9: geneseqm2003bs:*
           10: geneseqm2003cs:*
           11: geneseqm2003ds:*
           12: geneseqm2004as:*
           13: geneseqm2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1513	100.0	870	9	ADA02737	Ada02737 Mouse Ccn
2	1513	100.0	870	10	ADB72475	Adb72475 Mouse Ccn
3	1513	100.0	870	10	ADC85217	Adc85217 Mouse Ccn
4	1513	100.0	870	12	ADM74332	Adm74332 Murine ca
5	1513	100.0	876	5	AAD02406	Aad02406 Mouse cyc
6	1513	100.0	1255	9	ADA02736	Mouse Ccn
7	1513	100.0	1255	10	ADB72474	Mouse Ccn
8	1513	100.0	1255	10	ADC85216	Mouse Ccn
9	1513	100.0	1255	12	ADM74331	Murine ca
10	1380	91.2	870	9	ADA02740	Human CCN
11	1380	91.2	870	10	ADB72478	Human CCN
12	1380	91.2	870	10	ADC85220	Human Ccn
13	1380	91.2	870	12	ADM74335	Human car
14	1380	91.2	873	5	AAD02407	Human cyc
15	1380	91.2	1129	10	ACA60565	DNA encod
16	1380	91.2	1898	10	ADD18442	Human pro
17	1380	91.2	1911	10	AAQ31874	Cyclin D2
18	1380	91.2	1911	11	ADI31696	Human cDN
19	1380	91.2	6478	6	ABK35484	Human end
20	1380	91.2	6478	6	ABL66613	Lung canc
21	1380	91.2	6478	6	ABV94470	Breast ca
22	1380	91.2	6478	6	ABN95109	Gene #160
23	1380	91.2	6478	10	ADA02739	Human CCN
24	1380	91.2	6478	10	ADB72477	Human CCN
25	1380	91.2	6478	10	ADC85219	Human Ccn
26	1380	91.2	6478	10	ADF81445	Leukaemia
27	1380	91.2	6478	10	ADH28853	Human chr
28	1380	91.2	6478	12	ADM74334	Human car
29	1380	91.2	6478	12	ADO19119	Human PRO
30	1380	91.2	6480	8	ACF34507	Gene enco
31	1380	91.2	6480	10	ADF76507	Novel hum
32	1380	91.2	6480	12	ADH17148	Human cyc
33	1380	91.2	6480	12	ADL82848	Human PRO
34	1380	91.2	6480	12	ADP07302	Human CCN
35	1380	91.2	6480	12	ADO20473	Human PRO
36	1380	91.2	6480	12	ADO19115	Human PRO
37	1380	91.2	6480	12	ADO19117	Human PRO
38	1380	91.2	6480	13	ADP54150	Human PRO
39	1380	91.2	6480	13	ADP23073	PRO polyp
40	1380	91.2	6508	8	ABX63004	Human cDN
41	1380	91.2	6508	10	ADJ56260	Human cDN
42	1377	91.0	1911	2	AAQ53198	Human cyc
43	1374	90.8	6598	10	ADF81443	Leukaemia
44	1374	90.8	6598	10	ADF81444	Leukaemia
45	1316	87.0	6518	4	AAH57370	Human hea

ALIGNMENTS

RESULT 1
ADA02737
ID   ADA02737 standard; cDNA; 870 BP.
XX
AC   ADA02737;
XX
DT   06-NOV-2003 (first entry)
XX
DE   Mouse Ccnd2 carcinoma associated coding sequence, SEQ ID NO:1255.
XX
KW   Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;
KW   prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
KW   gene; 88.
XX
OS   Mus sp.
XX
PN   WO200305146-A2.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-US041414.
XX
PR   26-DEC-2001; 2001US-00035832.
XX
PA   (SAGR-) SAGRES DISCOVERY.
XX
PI   Morris DW;
XX
DR   WPI; 2003-587068/55.

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OM protein - nucleic search, using frame_plus_p2n model

Run on:      July 13, 2005, 20:18:51 ; Search time 3658 Seconds
                                 (without alignments)
                           3007.265 Million cell updates/sec

Title:          US-10-024-066-4
Perfect score:  1501
Sequence:       1 MBLLCHEVDPVRRAVRDRNL..........KSEDELDQASTPTDVRDIDL 289

Scoring table:  BLOSUM62
                Xgapop  10.0 , Xgapext  0.5
                Ygapop  10.0 , Ygapext  0.5
                Fgapop   6.0 , Fgapext  7.0
                Delop    6.0 , Delext   7.0

Searched:       3439544 seqs, 1903213470 residues

Total number of hits satisfying chosen parameters:      68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgm2_1/USPTO_spool_h/US10024066/runat_13072005_141000_28054/app_query.fasta_1.910
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10024066 @CGN_1_1_4385 @runat_13072005_141000_28054 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_htc:*
                 4: gb_est3:*             )
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_gss1:*
                 9: gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	1501	100.0	870	9	AY412428	AY412428 Homo sapi
2	1380	91.9	870	9	AY412430	AY412430 Mus muscu
3	1297	86.4	863	7	CF553381	CF553381 AGENCOURT
4	1212.5	80.8	861	7	CR573818	CR573818 CR573818
5	1168	77.8	674	7	CN262199	CN262199 170006000
6	1143	76.1	856	7	CF256675	CF256675 pha001_f0
7	1132.5	75.4	783	7	CN536040	CN536040 UI-M-HSO-
8	1129	75.2	689	6	CA316248	CA316248 UI-M-FW0-
9	1129	75.2	851	5	BX851524	BX851524 BX851524

				Pred.	ID	Description
10	1128.5	75.2	977	5	BU516674	BU516674 AGENCOURT
11	1116.5	74.4	752	6	BY711059	BY711059 BY711059
12	1113	74.2	704	4	BM790686	BM790686 K-EST0070
13	1097	73.1	649	6	CD773466	CD773466 AGENCOURT
14	1097	73.1	679	7	CR553173	CR553173 CR553173
15	1086	72.4	904	7	CF553242	CF553242 AGENCOURT
16	1080.5	72.0	848	5	BU35987	BU35987 603477919
17	1078	71.8	779	7	CN052742	CN052742 Salamande
18	1059	70.6	922	5	BQ946062	BQ946062 AGENCOURT
19	1056	70.4	640	7	CN533599	CN533599 UI-M-HOO-
20 c	1050.5	70.0	870	5	BX748469	BX748469 BX748469
21	1047	69.8	635	5	CB433883	CB433883 610445 MA
22	1039.5	69.3	840	5	BU056722	BU056722 UI-M-FOO-
23	1036.5	69.1	758	5	CN533832	CN533832 UI-M-HSO-
24	1027.5	68.5	957	6	BY717548	BY717548 BY717548
25 c	1026.5	68.4	851	1	AI790687	AI790687 ul03d12.x
26	1024	68.2	778	7	CK794714	CK794714 AGENCOURT
27	1023	68.2	591	4	BG912396	BG912396 602808475
28	1017	67.8	974	5	BU408763	BU408763 603157571
29	1005	67.0	700	7	BE140010	BE140010 EST00513
30 c	1003.5	66.9	748	7	CK463097	CK463097 933967 MA
31	999	66.6	800	2	BF723846	BF723846 EST00659
32	993.5	66.2	616	7	CF906821	CF906821 A0502B03-
33	993	66.2	673	1	AL631535	AL631535 AL631535
34	976	65.0	879	6	CB588849	CB588849 AGENCOURT
35	975	65.0	925	7	CO647021	CO647021 ILLUMIGEN
36	972	64.8	869	5	BP143684	BP143684 BP143684
37	963.5	64.2	850	6	CB994029	CB994029 AGENCOURT
38	957	63.8	814	5	BP143934	BP143934 BP143934
39	952	63.4	607	4	BM790062	BM790062 K-EST0069
40	952	63.4	621	6	CB215938	CB215938 NISC_npll
41 c	950.5	63.3	714	7	CK451417	CK451417 904589 MA
42	950	63.3	565	1	AV589900	AV589900 AV589900
43	950	63.3	867	6	CB994606	CB994606 AGENCOURT
44	949	63.2	593	1	AV593772	AV593772 AV593772
45	948.5	63.2	568	7	CF908102	CF908102 A0518G09-

ALIGNMENTS

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RESULT 1
AY412428
LOCUS        AY412428              870 bp    DNA       linear   GSS 16-DEC-2003
DEFINITION   Homo sapiens CCND2 gene, VIRTUAL TRANSCRIPT, partial sequence,
             genomic survey sequence.
ACCESSION    AY412428
VERSION      AY412428.1  GI:39768393
KEYWORDS     GSS.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 870)
AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
TITLE        Inferring nonneutral evolution from human-chimp-mouse orthologous
             gene trios
JOURNAL      Science 302 (5652), 1960-1963 (2003)
PUBMED       14671302
REFERENCE    2  (bases 1 to 870)
AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
TITLE        Direct Submission
JOURNAL      Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
             Rockville, MD 20850, USA
COMMENT      This sequence was made by sequencing genomic exons and ordering
             them based on alignment.
FEATURES             Location/Qualifiers
     source          1..870
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 13, 2005, 23:40:22 ; Search time 669.5 Seconds
(without alignments)
2710.137 Million cell updates/sec

Title: US-10-024-066-4
Perfect score: 1501
Sequence: 1 MELLCHEVDPVRRAVRDRNL.........KSEDELDQASTPTDVRDIDL 289

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 630947 seqs, 3139163630 residues

Total number of hits satisfying chosen parameters: 12661894

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DRV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10024066/runat_13072005_141002_28138/app_query.fasta_1.910
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10024066 @CGN_1_1_582 @runat_13072005_141002_28138
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1501	100.0	870	11	US-09-997-722-6	Sequence 6, Appli
2	1501	100.0	873	13	US-10-024-066-3	Sequence 3, Appli
3	1501	100.0	1898	16	US-10-210-120-14	Sequence 14, Appl
4	1501	100.0	1898	22	US-10-909-035-14	Sequence 14, Appl
5	1501	100.0	1911	18	US-10-641-643-1022	Sequence 1022, Ap
6	1501	100.0	6478	9	US-09-919-497-4	Sequence 4, Appli
7	1501	100.0	6478	9	US-09-954-456-1923	Sequence 1923, Ap
8	1501	100.0	6478	9	US-09-880-107-1607	Sequence 1607, Ap
9	1501	100.0	6478	11	US-09-997-722-5	Sequence 5, Appli
10	1501	100.0	6478	15	US-10-171-581-121	Sequence 121, App
11	1501	100.0	6478	15	US-10-007-926A-461	Sequence 461, App
12	1501	100.0	6478	21	US-10-843-641A-4950	Sequence 4950, Ap
13	1501	100.0	6480	17	US-10-440-464-147	Sequence 147, App
14	1501	100.0	6480	20	US-10-370-715B-181	Sequence 181, App
15	1501	100.0	6480	21	US-10-489-740-62	Sequence 62, Appl
16	1501	100.0	6508	15	US-10-044-090-4	Sequence 4, Appli
17	1501	100.0	6508	15	US-10-084-817-66	Sequence 66, Appl
18	1380	91.9	870	11	US-09-997-722-3	Sequence 3, Appli
19	1380	91.9	876	13	US-10-024-066-1	Sequence 1, Appli
20	1380	91.9	1255	11	US-09-997-722-2	Sequence 2, Appli
21	998	66.5	1053	9	US-09-778-927A-12	Sequence 12, Appl
22	925	61.6	4242	11	US-10-641-643-1365	Sequence 1365, Ap
23	925	61.6	4244	9	US-09-964-82A-566	Sequence 566, App
24	925	61.6	4244	9	US-09-954-456-1594	Sequence 1594, Ap
25	925	61.6	4244	9	US-09-967-768A-213	Sequence 213, App
26	925	61.6	4244	21	US-10-843-641A-4621	Sequence 4621, Ap
27	925	61.6	4244	21	US-10-843-641A-5869	Sequence 5869, Ap
28	925	61.6	4244	21	US-10-843-641A-6358	Sequence 6358, Ap
29	925	61.6	4306	17	US-10-295-027-635	Sequence 635, App
30	925	61.6	4306	18	US-10-302-812-67	Sequence 67, Appl
31	925	61.6	4397	17	US-10-264-049-423	Sequence 423, Appl
32	913	60.8	888	16	US-10-004-113-27	Sequence 27, Appl
33	913	60.8	888	16	US-10-004-113-30	Sequence 30, Appl
34	913	60.8	888	17	US-10-394-948-15	Sequence 15, Appl
35	913	60.8	888	17	US-10-394-948-18	Sequence 18, Appl
36	913	60.8	1256	21	US-10-690-880-10	Sequence 10, Appl
37	913	60.8	1325	15	US-10-007-926A-10	Sequence 10, Appl
38	913	60.8	1325	15	US-10-101-510-279	Sequence 279, App
39	913	60.8	1325	16	US-10-004-113-29	Sequence 29, Appl
40	913	60.8	1325	17	US-10-133-937-5	Sequence 5, Appli
41	913	60.8	1325	17	US-10-172-118-661	Sequence 661, App
42	913	60.8	1325	17	US-10-159-563-5	Sequence 5, Appli
43	913	60.8	1325	17	US-10-394-948-17	Sequence 17, Appl
44	913	60.8	1325	18	US-10-342-887-661	Sequence 661, App
45	913	60.8	1454	18	US-10-152-319A-2187	Sequence 2187, Ap

ALIGNMENTS

RESULT 1
US-09-997-722-6

; Sequence 6, Application US/09997722
; Publication No. US20040072154A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301

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                    GenCore version 5.1.6
         Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:    July 13, 2005, 20:22:56 ; Search time 189 Seconds
                         (without alignments)
                         2502.032 Million cell updates/sec

Title:         US-10-024-066-4
Perfect score: 1501
Sequence:      1 MBLLCHEVDPVRRAVRDRNL..........KSEDELDQASTPTDVRDIDL 289

Scoring table: BLOSUM62
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         Ygapop 10.0 , Ygapext   0.5
         Fgapop  6.0 , Fgapext   7.0
         Delop   6.0 , Delext    7.0

Searched:      1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:     2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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    6: /cgm2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                         SUMMARIES
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Result No.	Score	Query Match	Length	DB	ID	Description
1	1501	100.0	1129	4	US-09-920-760-3	Sequence 3, Appli
2	1501	100.0	1911	2	US-08-246-361A-3	Sequence 3, Appli
3	1501	100.0	1911	4	US-09-023-655-1022	Sequence 1022, Ap
4	1501	100.0	6478	4	US-09-919-497-4	Sequence 4, Appli
5	1501	100.0	6478	4	US-09-949-016-256	Sequence 256, App
6	1501	100.0	6479	2	US-09-949-016-2149	Sequence 2149, Ap
7	1471	98.0	1970	3	US-08-464-517-3	Sequence 3, Appli
8	1471	98.0	1970	3	US-08-463-772-3	Sequence 3, Appli
9	1471	98.0	1970	5	PCT-US93-05000-3	Sequence 3, Appli
10	1051.5	70.1	1462	2	US-08-464-517-30	Sequence 30, Appl
11	1051.5	70.1	1462	2	US-08-246-361A-30	Sequence 30, Appl
12	1051.5	70.1	1462	3	US-08-463-772-30	Sequence 30, Appl

13	1024.5	68.3	1462	5	PCT-US93-05000-30	Sequence 30, Appl
14	927	61.8	4453	1	US-08-770-761A-4	Sequence 4, Appli
15	927	61.8	4540	1	US-08-770-761A-6	Sequence 6, Appli
16	927	61.8	4621	1	US-08-770-761A-1	Sequence 1, Appli
17	925	61.6	4221	1	US-07-947-120-7	Sequence 7, Appli
18	925	61.6	4221	1	US-08-472-893A-7	Sequence 7, Appli
19	925	61.6	4221	3	US-08-947-492-7	Sequence 7, Appli
20	925	61.6	4242	4	US-09-023-655-1365	Sequence 1365, Ap
21	925	61.6	4244	4	US-08-460-694-1	Sequence 1, Appli
22	925	61.6	4244	3	US-08-460-744-1	Sequence 1, Appli
23	925	61.6	4244	3	US-07-667-711B-1	Sequence 1, Appli
24	913	60.8	1325	1	US-08-306-691B-51	Sequence 51, Appli
25	911.5	60.7	1962	2	US-08-246-361A-5	Sequence 5, Appli
26	911.5	60.7	1962	4	US-09-023-655-1023	Sequence 1023, Ap
27	911.5	60.7	2042	4	US-09-814-915A-59	Sequence 59, Appl
28	865	57.6	1325	2	US-08-464-517-1	Sequence 1, Appli
29	865	57.6	1325	2	US-08-246-361A-1	Sequence 1, Appli
30	865	57.6	1325	3	US-08-463-772-1	Sequence 1, Appli
31	865	57.6	1325	5	PCT-US93-05000-1	Sequence 1, Appli
32	801.5	53.4	1926	2	US-08-464-517-5	Sequence 5, Appli
33	801.5	53.4	1926	5	US-08-463-772-5	Sequence 5, Appli
34	801.5	53.4	1926	5	PCT-US93-05000-5	Sequence 5, Appli
35	522	34.8	2022	2	US-08-464-517-32	Sequence 32, Appl
36	522	34.8	2022	2	US-08-246-361A-32	Sequence 32, Appl
37	522	34.8	2022	3	US-08-463-772-32	Sequence 32, Appl
38	426	28.4	1901	2	PCT-US93-05000-32	Sequence 32, Appl
39	377.5	25.1	36302	4	US-09-949-016-11998	Sequence 11998, A
40	377.5	25.1	36302	4	US-09-949-016-13891	Sequence 13891, A
41	314.5	21.0	863	3	US-08-728-603-18	Sequence 18, Appl
c	42	314.5	21.0	32207	3	US-08-770-379-20	Sequence 20, Appl
c	43	314.5	21.0	32207	3	US-08-757-669A-20	Sequence 20, Appl
c	44	314.5	21.0	32207	3	US-09-230-371A-20	Sequence 20, Appl
45	280.5	18.7	601	4	US-09-949-016-23242	Sequence 23242, A

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                         ALIGNMENTS

RESULT 1
US-09-920-760-3
; Sequence 3, Application US/09920760
; Patent No. 6492173
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN D2 EXPRESSION
;  FILE REFERENCE: RTS-0275
;  CURRENT APPLICATION NUMBER: US/09/920,760
;  CURRENT FILING DATE: 2001-08-01
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
;  LENGTH: 1129
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (156)...(1025)
US-09-920-760-3

Alignment Scores:
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Score:                   1501.00       Matches:          289
Percent Similarity:      100.00%       Conservative:     0
Best Local Similarity:   100.00%       Mismatches:       0
Query Match:             100.00%       Indels:           0
DB:                      4             Gaps:             0

US-10-024-066-4 (1-289)  x US-09-920-760-3 (1-1129)

Qy     1 MetGluLeuLeuCysHisGluValAspProValArgArgAlaValArgAspArgAsnLeu 20
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Db   156 ATGGAGCTGCTGTGCCACGAGGTGGACCCGGTCCGCAGGGCCGTGCGGGACCGCAACCTG 215

Qy    21 LeuArgAspAspArgValLeuGlnAsnLeuGluThrLeuGluGluArgTyrLeuProGln 40
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OM protein - nucleic search, using frame_plus_p2n model

Run on:  July 13, 2005, 17:34:44 ; Search time 596.5 Seconds
                                    (without alignments)
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Title:          US-10-024-066-4
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Searched:       4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:        8780412

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1501	100.0	870	9	ADA02740	Ada02740 Human CCN
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3	1501	100.0	870	10	ADC85220	Adc85220 Human Ccn
4	1501	100.0	870	12	ADM74335	Adm74335 Human car
5	1501	100.0	873	5	AAD02407	Aad02407 Human cyc
6	1501	100.0	1129	10	ACA60565	Aca60565 DNA encod
7	1501	100.0	1898	10	ADD18442	Add18442 Human pro
8	1501	100.0	1911	2	AAQ31874	Aaq31874 Cyclin D2
9	1501	100.0	1911	11	ADI31696	Adi31696 Human cDN
10	1501	100.0	6478	6	ABK35484	Abk35484 Human end
11	1501	100.0	6478	6	ABL66613	Abl66613 Lung canc
12	1501	100.0	6478	6	ABV94470	Abv94470 Breast ca
13	1501	100.0	6478	6	ABN95109	Abn95109 Gene #160
14	1501	100.0	6478	9	ADA02739	Ada02739 Human CCN
15	1501	100.0	6478	10	ADB72477	Adb72477 Human CCN
16	1501	100.0	6478	10	ADC85219	Adc85219 Human Ccn
17	1501	100.0	6478	10	ADF81445	Adf81445 Leukaemia
18	1501	100.0	6478	10	ADH28853	Adh28853 Human chr
19	1501	100.0	6478	12	ADM74334	Adm74334 Human car
20	1501	100.0	6478	12	ADO19119	Ado19119 Human PRO
21	1501	100.0	6480	8	ACF34507	Acf34507 Gene enco
22	1501	100.0	6480	12	ADF76507	Adf76507 Novel hum
23	1501	100.0	6480	12	ADH17148	Adh17148 Human cyc
24	1501	100.0	6480	12	ADL82848	Adl82848 Human PRO
25	1501	100.0	6480	12	ADP07302	Adp07302 Human CCN
26	1501	100.0	6480	12	ADO20473	Ado20473 Human PRO
27	1501	100.0	6480	12	ADO19115	Ado19115 Human PRO
28	1501	100.0	6480	12	ADO19117	Ado19117 Human PRO
29	1501	100.0	6480	13	ADP54150	Adp54150 Human PRO
30	1501	100.0	6480	13	ADP23073	Adp23073 PRO polyp
31	1501	100.0	6508	8	ABX63004	Abx63004 Human cDN
32	1501	100.0	6508	10	ADJ56260	Adj56260 Human cDN
33	1495	99.6	6598	10	ADF81443	Adf81443 Leukaemia
34	1491	99.3	6598	10	ADF81444	Adf81444 Leukaemia
35	1436	95.7	1911	2	AAQ53198	Aaq53198 Human hea
36	1436	95.7	6518	4	AAH57370	Aah57370 Human hea
37	1380	91.9	870	10	ADA02737	Ada02737 Mouse Ccn
38	1380	91.9	870	10	ADB72475	Adb72475 Mouse Ccn
39	1380	91.9	870	10	ADC85217	Adc85217 Mouse Ccn
40	1380	91.9	870	12	ADM74332	Adm74332 Murine ca
41	1380	91.9	876	12	AAD02406	Aad02406 Mouse cyc
42	1380	91.9	1255	9	ADA02736	Ada02736 Mouse Ccn
43	1380	91.9	1255	10	ADB72474	Adb72474 Mouse Ccn
44	1380	91.9	1255	10	ADC85216	Adc85216 Mouse Ccn
45	1380	91.9	1255	12	ADM74331	Adm74331 Murine ca

ALIGNMENTS

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AC   ADA02740;
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DT   06-NOV-2003  (first entry)
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DE   Human CCND2 carcinoma associated coding sequence, SEQ ID NO:1258.
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KW   Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
KW   prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200305146-A2.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-US041414.
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PR   26-DEC-2001; 2001US-00035832.
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PA   (SAGR-) SAGRES DISCOVERY.
XX
PI   Morris DW;
XX
DR   WPI; 2003-587068/55.
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on:　July 13, 2005, 19:05:08 ; Search time 4889.5 Seconds
　　　　　　　　　　　　　　　　　(without alignments)
　　　　　　　　　　　　　　　　2864.006 Million cell updates/sec

Title:　　　　　US-10-024-066-4
Perfect score:　1501
Sequence:　　　1 MELLCHEVDPVRRAVRDRNL.........KSEDELDQASTPTDVRDIDL 289

Scoring table:　BLOSUM62
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　　　　　　Ygapop 10.0 , Ygapext　0.5
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　　　　　　Delop　 6.0 , Delext　 7.0

Searched:　　　4708233 seqs, 2422607955 residues

Total number of hits satisfying chosen parameters:　　9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
　　　　　　　　 Maximum Match 100%
　　　　　　　　 Listing first 45 summaries

Command line parameters:
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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10024066 @CGN_1_1_4930 @runat_13072005_140959_28043 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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　　　6: gb_pat:*
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　　　10: gb_ro:*
　　　11: gb_sts:*
　　　12: gb_sy:*
　　　13: gb_un:*
　　　14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
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4	1501	100.0	1344	9	BC010958	BC010958 Homo sapi

5	1501	100.0	1911	6	AR093074	AR093074 Sequence
6	1501	100.0	1911	6	AR380477	AR380477 Sequence
7	1501	100.0	1911	6	BD079953	BD079953 Use relat
8	1501	100.0	1911	9	HUMCCND2A	M90813 Human D-typ
9	1501	100.0	6478	6	AX334441	AX334441 Sequence
10	1501	100.0	6478	6	AX408960	AX408960 Sequence
11	1501	100.0	6478	6	AX587991	AX587991 Sequence
12	1501	100.0	6478	6	AX695630	AX695630 Sequence
13	1501	100.0	6478	6	AX779844	AX779844 Sequence
14	1501	100.0	6478	9	HUMRSC289	D13639 Homo sapien
15	1495	99.6	6598	6	AX779842	AX779842 Sequence
16	1495	99.6	6598	6	AX779843	AX779843 Sequence
17	1471	98.0	1970	6	AR034831	AR034831 Sequence
18	1402.5	93.4	1230	4	AB046174	AB046174 Sus scrof
19	1392.5	92.8	1415	10	RATCYCLD2A	L09752 Rat cyclin
20	1380	91.9	870	6	AX695628	AX695628 Sequence
21	1380	91.9	1034	10	MUSCYL2A	M86182 Mouse cycli
22	1380	91.9	1255	6	AX695627	AX695627 Sequence
23	1380	91.9	1255	10	MUSDCYC	M83749 Mouse D-typ
24	1380	91.9	2037	10	BC049086	BC049086 Mus muscu
25	1379.5	91.9	1120	10	RATCLND2	D16308 Rattus norv
26	1256	83.7	1173	5	GGU28980	U28980 Gallus gall
27	1236	82.3	1588	5	XLCYCLND2	X89476 X.laevis mR
28	1236	82.3	2038	5	XLCYCD2	X83503 X.laevis mR
29	1083.5	72.2	170682	2	AC073256	AC073256 Homo sapi
30	1067.5	71.1	160945	9	AP003420	AP003420 Homo sapi
31	1066.5	71.1	116273	2	AP000596	AP000596 Homo sapi
32	1062.5	70.8	169776	9	AP001880	AP001880 Homo sapi
33	1062.5	70.8	169777	2	AC090778	AC090778 Homo sapi
34	1058.5	70.5	185404	2	AC025409	AC025409 Homo sapi
35	1051.5	70.1	1462	6	AR034838	AR034838 Sequence
36	1051.5	70.1	1462	6	AR093081	AR093081 Sequence
37	1051.5	70.1	1462	6	BD079960	BD079960 Use relat
38	1024.5	68.3	1462	9	HUMCCND2PS	M91003 Human pseud
39	953.5	63.5	2248	5	AJ720095	AJ720095 Gallus ga
40	927	61.8	4453	2	AR043602	AR043602 Sequence
41	927	61.8	4540	6	AR043603	AR043603 Sequence
42	927	61.8	4621	6	AR043601	AR043601 Sequence
43	925	61.6	885	9	CR542099	CR542099 Homo sapi
44	925	61.6	888	9	CR536538	CR536538 Homo sapi
45	925	61.6	1248	9	BC014078	BC014078 Homo sapi

ALIGNMENTS

RESULT 1
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DEFINITION　　Sequence 1258 from Patent WO03008583.
ACCESSION　　 AX695631
VERSION　　　　AX695631.1　GI:29418783
KEYWORDS　　　.
SOURCE　　　　 Homo sapiens (human)
　ORGANISM　　 Homo sapiens
　　　　　　　 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
　　　　　　　 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE　　 1
AUTHORS　　　 Morris,D.W. and Engelhard,E.K.
TITLE　　　　 Novel compositions and methods for cancer
JOURNAL　　　 Patent: WO 03008583-A 1258 30-JAN-2003;
　　　　　　　 Sagres Discovery (US)
FEATURES　　　　　　　　　　　　　Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:　　　　　　　　 9.43e-147　　　Length:　　　　　　　870
Score:　　　　　　　　　　 1501.00　　　 Matches:　　　　　　289
Percent Similarity:　　　 100.00%　　　 Conservative:　　　　0
Best Local Similarity:　　100.00%　　　 Mismatches:　　　　　0

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 13, 2005, 19:05:08 ; Search time 4889.5 Seconds
           (without alignments)
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Title: US-10-024-066-2
Perfect score: 1513
Sequence: 1 MELLCCEVDPVRRAVPDRNL........KSVEDPDQATTPTPVRDVDL 289

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                Ygapop 10.0 , Ygapext 0.5
                Fgapop   6.0 , Fgapext 7.0
                Delop   6.0 , Delext   7.0

Searched: 4708233 seqs, 2427607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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SUMMARIES

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         12:   gb_sy:*
         13:   gb_un:*
         14:   gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	1513	100.0	870	6	AX695628	AX695628 Sequence
2	1513	100.0	1034	10	MUSCYL2A	M86182 Mouse cycli
3	1513	100.0	1255	6	AX695627	AX695627 Sequence
4	1513	100.0	1255	10	MUSDCYC	M83749 Mouse D-typ
5	1513	100.0	2037	10	BC049086	BC049086 Mus muscu
6	1482.5	98.0	1415	10	RATCYCLD2A	L09752 Rat cyclin
7	1469.5	97.1	1120	10	RATCLND2	D16308 Rattus norv
8	1380	91.2	870	6	AX695631	AX695631 Sequence
9	1380	91.2	1129	6	AR266191	AR266191 Sequence
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11	1380	91.2	1344	9	BC010958	BC010958 Homo sapi
12	1380	91.2	1911	6	AR093074	AR093074 Sequence
13	1380	91.2	1911	6	AR380477	AR380477 Sequence
14	1380	91.2	1911	6	BD079953	BD079953 Use relat
15	1380	91.2	1911	9	HUMCCND2A	M90813 Human D-typ
16	1380	91.2	6478	6	AX334441	AX334441 Sequence
17	1380	91.2	6478	6	AX408960	AX408960 Sequence
18	1380	91.2	6478	6	AX587991	AX587991 Sequence
19	1380	91.2	6478	6	AX695630	AX695630 Sequence
20	1380	91.2	6478	6	AX779844	AX779844 Sequence
21	1380	91.2	6478	9	HUMRSC289	D13639 Homo sapien
22	1374	90.8	6598	6	AX779842	AX779842 Sequence
23	1374	90.8	6598	6	AX779843	AX779843 Sequence
24	1360.5	89.9	1230	4	AB046174	AB046174 Sus scrof
25	1357	89.7	1970	6	AR034831	AR034831 Sequence
26	1267	83.7	1173	5	GGU28980	U28980 Gallus gall
27	1225	81.0	1588	5	XLCYCLND2	X89476 X.laevis mR
28	1225	81.0	2038	5	XLCYCD2	X83503 X.laevis mR
c 29	1007.5	66.6	170682	2	AC073256	AC073256 Homo sapi
30	991.5	65.5	160945	2	AP003420	AP003420 Homo sapi
c 31	988.5	65.3	116273	2	AP000596	AP000596 Homo sapi
32	986.5	65.2	169776	9	AP001880	AP001880 Homo sapi
c 33	986.5	65.2	169777	2	AC090778	AC090778 Homo sapi
c 34	979.5	64.7	185404	2	AC025409	AC025409 Homo sapi
35	975.5	64.5	1462	6	AR034838	AR034838 Sequence
36	975.5	64.5	1462	6	AR093081	AR093081 Sequence
37	975.5	64.5	1462	6	BD079960	BD079960 Use relat
38	961	63.5	1555	5	BC074566	BC074566 Xenopus t
39	958	63.3	885	9	CR542099	CR542099 Homo sapi
40	958	63.3	888	9	CR536538	CR536538 Homo sapi
41	958	63.3	1248	9	BC014078	BC014078 Homo sapi
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ALIGNMENTS

RESULT 1
AX695628

LOCUS   AX695628   870 bp   DNA   linear   PAT 31-MAR-2003
DEFINITION Sequence 1255 from Patent WO03008583.
ACCESSION   AX695628
VERSION   AX695628.1 GI:29418780
KEYWORDS   .
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Morris,D.W. and Engelhard,E.K.
  TITLE   Novel compositions and methods for cancer
  JOURNAL   Patent: WO 03008583-A 1255 30-JAN-2003;
            Sagres Discovery (US)
FEATURES   Location/Qualifiers
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ORIGIN

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Best Local Similarity: 100.00%   Mismatches: 0